

5'	NNG	CGG	CCT	CTG	ACA	CCA	GCA	CAG	CAA	ACC	CGC	CGG	GAT	CAA	AGT	GTA	CCA	GTC	54
X	R	P	L	T	P	A	Q	Q	T	R	R	R	D	Q	S	V	P	V	45
G	S	M	A	T	K	C	G	N	C	G	P	G	Y	S	T	P	L	108	
63	GGC	AGC	ATG	GCT	ACG	AAA	TGT	GGG	AAT	TGT	GGA	CCC	GGC	TAC	TCC	ACC	CCT	CTG	9
G	S	M	A	T	K	C	G	N	C	G	P	G	Y	S	T	P	L	99	
117	GAG	GCC	ATG	AAA	GGA	CCC	AGG	GAA	GAG	ATC	GTC	TAC	CTG	CCC	TGC	ATT	TAC	CGA	27
E	A	M	K	G	P	R	E	E	I	V	Y	L	P	C	I	Y	R	162	
171	AAC	ACA	GGC	ACT	GAG	GCC	CCA	GAT	TAT	CTG	GCC	ACT	GTG	GAT	GTT	GAC	CCC	AAG	81
N	T	G	T	E	A	P	D	Y	L	A	T	V	D	V	D	P	K	189	
225	TCT	CCC	CAG	TAT	TGC	CAG	GTC	ATC	CAC	CGG	CTG	CCC	ATG	CCC	AAC	CTG	AAG	GAC	198
S	P	Q	Y	C	Q	V	I	H	R	L	P	M	P	N	L	K	D	207	
279	GAG	CTG	CAT	CAC	TCA	GGG	TGG	AAC	ACC	TGC	AGC	TGC	TTC	GGT	GAT	AGC	ACC	216	
E	L	H	H	S	G	W	N	T	C	S	S	C	F	G	D	S	T	297	
333	AAG	TCG	CGC	ACC	AAG	CTG	GTG	CTG	CCC	AGT	CTC	ATC	TCC	TCT	CGC	ATC	TAT	GTG	306
K	S	R	T	K	L	V	L	P	S	L	I	I	S	S	R	I	Y	V	315

FIGURE 1A

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387	GTC	GAC	GTG	GGC	TCT	GAG	CCC	CGG	GCC	CCA	AAG	CTG	CAC	AAG	GTC	ATT	GAG	CCC	432
V	D	V	G	S	E	P	R	A	P	K	L	H	K	V	I	E	P		
441	AAG	GAC	ATC	CAT	GCC	AAG	TGC	GAA	CTG	GCC	TTT	CTC	CAC	ACC	AGC	CAC	TGC	CTG	486
K	D	I	H	A	K	C	E	L	A	F	L	H	T	S	H	C	L		
495	GCC	AGC	GGG	GAA	GTG	ATG	ATC	AGC	TCC	CTG	GGA	GAC	GTC	AAG	GGC	AAT	GGC	AAA	540
A	S	G	E	V	M	I	S	S	L	G	D	V	K	G	N	G	K		
549	GGG	GGT	TTT	GTG	CTG	GAT	GGG	GAG	ACG	TTC	GAG	GTG	AAG	GGG	ACA	TGG	GAG	594	
G	G	F	V	L	L	D	G	E	T	F	E	V	K	G	T	W	E		
603	AGA	CCT	GGG	GGT	GCT	GCA	CCG	TTG	GGC	TAT	GAC	TTC	TGG	TAC	CAG	CCT	CGA	CAC	648
R	P	G	G	A	A	P	L	G	Y	D	F	W	Y	Q	P	R	H		
657	AAT	GTC	ATG	ATC	AGC	ACT	GAG	TGG	GCA	GCT	CCC	AAT	GTC	TTA	CGA	GAT	GGC	TTC	702
N	V	M	I	S	T	E	W	A	A	P	N	V	L	R	D	G	F		
711	AAC	CCC	GCT	GAT	GTG	GAG	GCT	GGA	CTG	TAC	GGG	AGC	CAC	TTA	TAT	GTA	TGG	GAC	756
N	P	A	D	V	E	A	G	L	Y	G	S	H	L	Y	V	W	D		

FIGURE 1B

W	Q	R	H	E	I	V	Q	T	L	S	L	K	D	G	L	I	P
765		774		783							792			801			810
TGG	CAG	CGC	CAT	GAG	ATT	GTG	CAG	ACC	CTG	TCT	CTA	AAA	GAT	GGG	CTT	ATT	CCC
L	E	I	R	F	L	H	N	P	D	A	A	Q	G	F	V	G	C
819		828		837							846			855			864
TTG	GAG	ATC	CGC	TTC	CTG	CAC	AAC	CCA	GAC	GCT	GCC	CAA	GGC	TTT	GTG	GGC	TGC
A	L	S	S	T	I	Q	R	F	Y	K	N	E	G	G	T	W	S
873		882		891							900			909			918
GCA	CTC	AGC	TCC	ACC	ATC	CAG	CGC	TTC	TAC	AAG	AAC	GAG	GGA	GGT	ACA	TGG	TCA
V	E	K	V	I	Q	V	P	P	K	K	V	K	W	L	L	P	
927		936		945							954			963			972
GTG	GAG	AAG	GTG	ATC	CAG	GTG	CCC	CCC	AAG	AAA	GTG	AAG	GGC	TGG	CTG	CTG	CCC
E	M	P	G	L	I	T	D	I	L	L	S	L	D	D	R	F	L
981		990		999							1008			1017			1026
GAA	ATG	CCA	GGC	CTG	ATC	ACC	GAC	ATC	CTG	CTC	TCC	CTG	GAC	CGC	TTC	CTC	
Y	F	S	N	W	L	H	G	D	L	R	Q	Y	D	I	S	D	P
1035		1044		1053							1062			1071			1080
TAC	TTC	AGC	AAC	TGG	CTG	CAT	GGG	GAC	CTG	AGG	CAG	TAT	GAC	ATC	TCT	GAC	CCA
Q	R	P	R	L	T	G	Q	L	F	L	G	S	I	V	K	G	

FIGURE 1C

3 of 10

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1143	GGC CCT GTG CAA GTG CTG GAG GAC GAG GAA CTA AAG TCC CAG CCA GAG CCC CTA	1152	1152	1161	1161	1170	1179	1188
G	P V Q V L E D E E L K S Q P E P L							
1197	GTG GTC AAG GGA AAA CGG GTG GCT GGA GGC CCT CAG ATG ATC CAG CTC AGC CTG	1206	1206	1215	1224	1233	1242	
V	V K G K R V A G G P Q M I Q L S L							
1251	GAT GGG AAG CGC CTC TAC ATC ACC ACG TCG CTG TAC AGT GCC TGG GAC AAG CAG	1260	1269	1278	1287	1296	1296	
D	G K R L Y I T T S L Y S A W D K Q							
1305	TCT TAC CCT GAT CTC ATC AGG GAA GGC TCT GTG ATG CTG CAG GTT GAT GTA GAC	1314	1323	1332	1341	1350	1350	
F	Y P D L I R E G S V M L Q V D V D							
1359	ACA GTA AAA GGA GGG CTG AAG TTG AAC CCC AAC TTC CTG GTG GAC TTC GGG AAG	1368	1377	1386	1395	1404	1404	
T	V K G G L K L N P N F L V D F G K							
1413	GAG CCC CTT GCC CCA GCC CTT GCC CAT GAG CTC CGC TAC CCT GGG GGC GAT TGT	1422	1431	1440	1449	1458	1458	
E	P L G P A L A H E L R Y P G G D C							
1467	AGC TCT GAC ATC TGG ATT TGA ACT CCA CCC TCA TCA CCC ACA CTC CCT ATT TTG	1476	1485	1494	1503	1512	1512	
S	S D I W I							

FIGURE 1D

GGC CCT CAC TTC CTT GGG GAC CTG GCT TCA TTC TGC TCT CTC TTG GCA CCC GAC
1521 1530 1539 1548 1557 1556
CCT TGG CAG CAT GTA CCA CAC AGC CAA GCT GAG ACT GTG GCA ATG TGT TGA GTC
1575 1584 1593 1602 1611 1620
ATA TAC ATT TAC TGA CCA CTG TTG CTT GTT GCT CAC TGT GCT GCT TTT CCA TGA
1629 1638 1647 1656 1665 1674
GCT CTT GGA GGC ACC AAG AAA TAA ACT CGT AAC CCT GTC 3'
1683 1692 1701 1710

FIGURE 1E

1	M A T K C G N C G P G Y S T P L E A M K G P R E E I V Y L P C I Y R N T G T E A	HSEBP
1	M A T K C G N C G P G Y S T P L E A M K G P R E E I V Y L P C I Y R N T G T E A	g1374792
1	M A T K C T K C G P G Y S T P L E A M K G P R E E I V Y L P C I Y R N T G T E A	g227630
1	M A T K C T K C G P G P S T P L E A M K G P R E E I V Y L P C I Y R N T G T E A	g298710
41	P D Y L A T V D V D P K S P Q Y C Q V I H R L P M P N L K D E L H H S G W N T C	HSEBP
41	P D Y L A T V D V D P K S P Q Y C Q V I H R L P M P N L K D E L H H S G W N T Y	g1374792
41	P D Y L A T V D V D P K S P Q Y S Q V I H R L P M P Y L K D E L H H S G W N T C	g227630
41	P D Y L A T V D V D P K S P Q Y S Q V I H R L P M P Y L K D E L H H S G W N T C	g298710
81	S S C F G D S T K S R T K L V L P S L I S S R I Y V V D V G S E P R A P K L H K	HSEBP
81	S S C F G D S T K S R N K L V L P S L I S S R I Y V V D V G S E P G P Q K L H K	g1374792
81	S S C F G D S T K S R N K L I L P G L I S S R I Y V V D V G S E P R A P K L H K	g227630
81	S S C F G D S T K S R N K L I L P G L M S S R I Y V V D V G S E P R A P K L H K	g298710
121	V I E P K D I H A K C E L A F L H T S H C L A S G E V M I S S L G D V K G N G K	HSEBP
121	V I E P K D I H A K C E L A C L H T S H C L A S G E V M I S S L G D V K G N G K	g1374792
121	V I E A S E I Q A K C N V S S L H T S H C L A S G E V M V S T I L G D I Q G N G K	g227630
121	V I E A S E I Q A K C N V S N T H T S H C L A S G E V M V S T I L G D I L Q G N G K	g298710
161	G G F V L L D G E T F E V K G T W E R P G G A A P L G Y D F W Y Q P R H N V M I	HSEBP
161	G G F V L L D G E T F E V K G T W E R P G G A A P L G Y D F W Y Q P R H N V M I	g1374792
161	G S F V L L D G E T F E V K G T W E K P G D A A P M G Y D F W Y Q P R H N V M V	g227630
161	G S F V L L D G E T F E V K G T W E K P G G A S P M G Y D F W Y Q P R H N V M V	g298710

FIGURE 2A

201	S T E W A A P N V L R D G F N P A D V E A G L Y G S H L Y V W D W Q R H E I V Q	HSEBP
201	S T E W A A P N V L R D G F N P A D V E A G L Y G S H L Y V W D W Q R H E I V Q	g1374792
201	S T E W A A P N V F K D G T N P A H V V E A G L Y G S R I F V W D W Q R H E I I Q	g227630
201	S T E W A A P N V F K D G F N P A H V V E A G L Y G S R I F V W D W Q R H E I I Q	g298710
241	T L S L K D G L I P L E I R F L H N P D A A Q G F V G C A L S S T I Q R F Y K N	HSEBP
241	T L S L K D G L I P L E I R F L H N P S A T Q G F V G C A S A P N I Q R F Y K T	HSEBP
241	T L Q M T D G L I P L E I R F L H D P S A T Q G F V G C A S A P N I Q R F Y K N	g1374792
241	T L Q M T D G L I P L E I R F L H D P S A T Q G F V G C A L S S N I Q R F Y K N	g227630
241	T L Q M T D G L I P L E I R F L H D P S A T Q G F V G C A L S S N I Q R F Y K N	g298710
281	E G G T W S V E K V I Q V P P K V K G W L L P E M P G L I T D I L L S L D D R	HSEBP
281	R E G T W S V E K V I Q V P P K V K G W L L P G V P G L I T D I L L S L D D R	HSEBP
281	A E G T W S V E K V I Q V P S K K V K G W M L P G V P G L I T D I L L S L D D R	g1374792
281	G E G T W S V E K V I Q V P S K K V K G W M L P E M P G L I T D I L L S L D D R	g227630
281	G E G T W S V E K V I Q V P S K K V K G W M L P E M P G L I T D I L L S L D D R	g298710
321	F L Y F S N W L H G D L R Q Y D I S D P Q R P R L T G Q L F L G G S I V K G G P	HSEBP
321	F L Y F S N W L H G D L R Q Y D I S D P Q R P R L T G Q L F L G G S I V K G G P	g1374792
321	F L Y F S N W L H G D I R Q Y D I S N P Q K P R L A G Q I F L G G S I V R G G S	g227630
321	F L Y F S N W L H G D I R Q Y D I S N P Q K P R L T G Q I F L G G S I V R G G S	g298710
361	V Q V L E D E E L K S Q P E P L V V K G K R V A G G P Q M I Q L S L D G K R L Y	HSEBP
361	V Q V L E D E E L K S Q P E P L V V K G K R V A G G P Q M I Q L S L D G K R L Y	g1374792
361	V Q V L E D Q E L T C Q P E P L V V K G K R I P G G P Q M I Q L S L D G K R L Y	g227630
361	V Q V L E D Q E L T C Q P E P L V V K G K R I P G G P Q M I Q L S L D G K R L Y	g298710

FIGURE 2B

401 I T T S L Y S A W D K Q F Y P D L I R E G S V M L Q V D V D T V K G G L K L N P
 HSEBP
 401 I T T S L Y S A W E K Q F Y P D L I R E G S V M L Q V D V D T V K G G L K L N P 91374792
 401 A T T S L Y S A W D K Q F Y P D L I R E G S M M L Q I D V D T V N G G L K L N P 9227630
 401 A T T S L Y S A W D K Q F Y P D L I R E G S V M L Q V D V D T V N G G L K L N P 9298710

441 N F L V D F G K E P L G P A L A H E L R Y P G G D C S S D I W I
 HSEBP
 441 N C L V D F G K E P L G P A L A H E L R Y P G G D C S S D I W I
 g1374792
 441 N F L V D F G K L P L G A A L A H E L R Y P G G D C S S D I W I
 g227630
 441 N F L V D F G K E P L G P A L A H E L R Y P G G D C S S D I W I
 g298710

FIGURE 2C

9 8 10

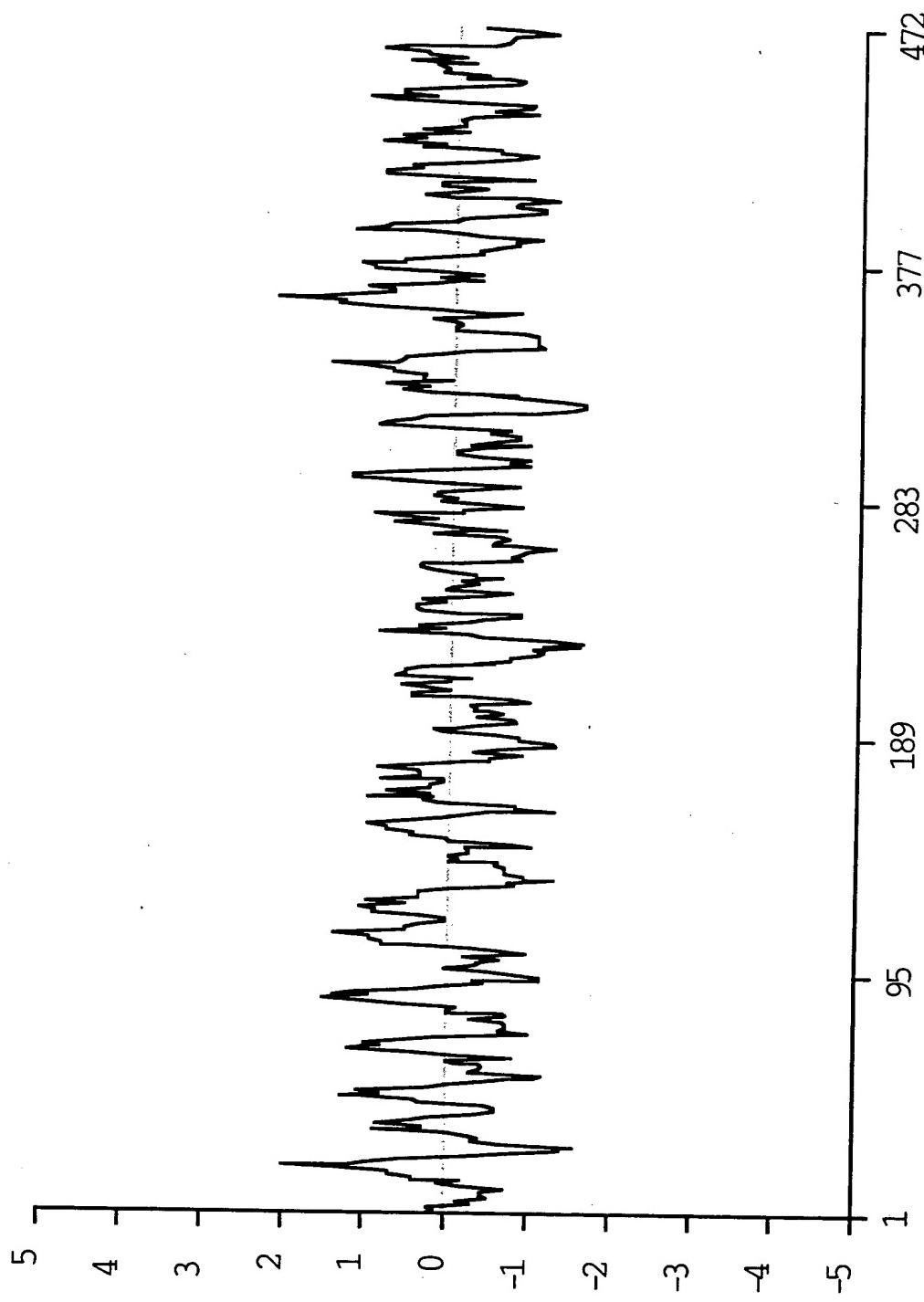


FIGURE 3

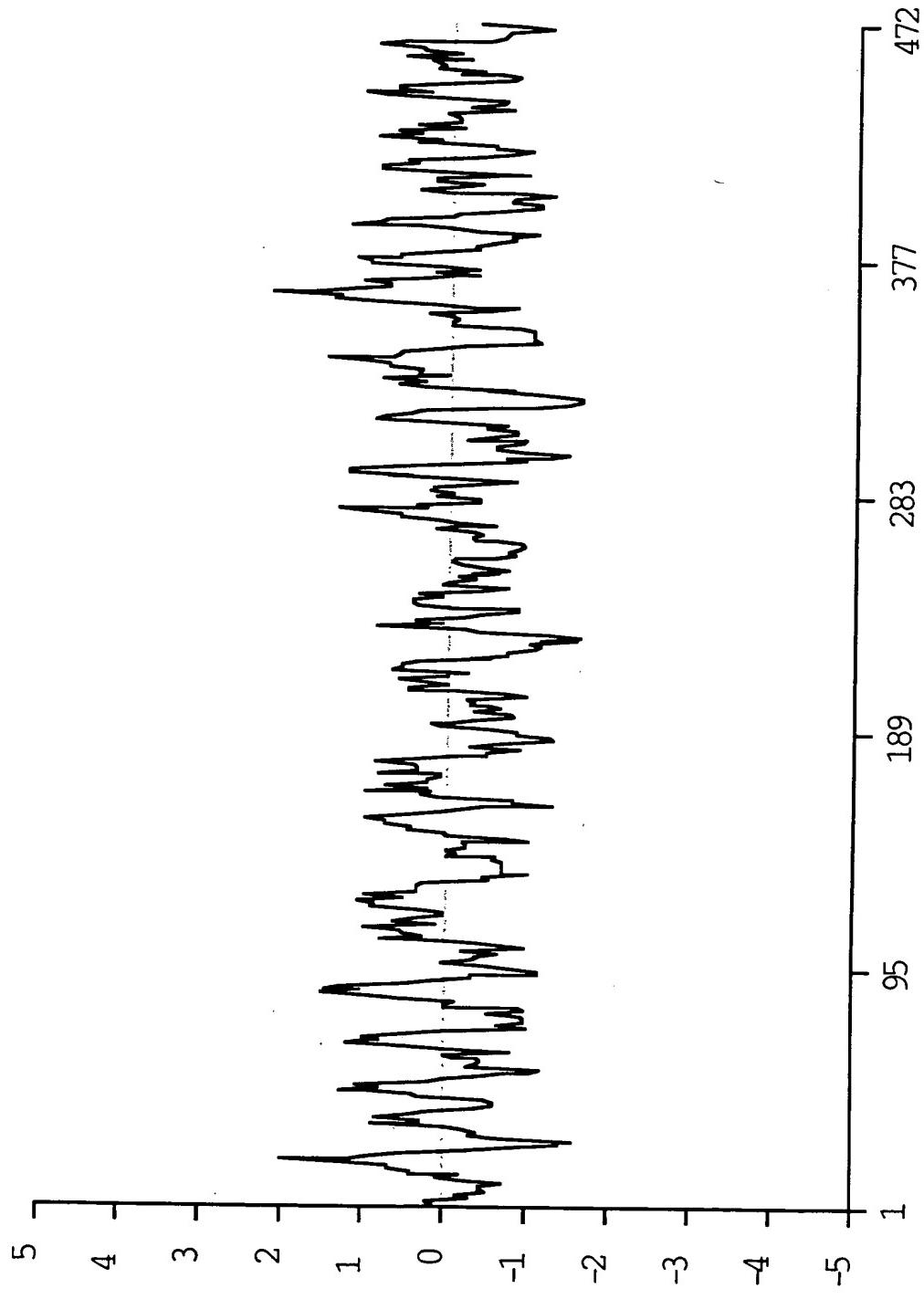


FIGURE 4

Library	Lib Description	Abun	Pct	Abun	Pct
COLNNOT13	colon, ascending, 28 M	2	0.0621		
PROSTUT01	prostate tumor, 50 M, match to PROSNOT02	2	0.0619		
COLNNOT16	colon, 62 M, match to COLNTUT03	2	0.0589		
COLNNOT11	colon, 60 M	1	0.0307		
TONGTUT01	tongue tumor, carcinoma, 36 M	1	0.0295		
PANCTUT01	pancreatic tumor, 65 F, match to PANCNOT08	1	0.0257		
COLNTUT02	colon tumor, 75 match to COLNNOT01	1	0.0220		
LUNGNOT03	lung, 79 M, match to LUNGUT02	1	0.0200		
LUNGUT02	lung tumor, metastasis, 79 M, match to LUNGNOT03	1	0.0188		
PROSTUT04	prostate tumor, 57 M, match to PROSNOT06	1	0.0163		
CORPNOT02	brain, corpus callosum, Alzheimer's, 74 M	1	0.0152		
LUNGAST01	lung, asthma, 17 M	1	0.0150		
THYRNOT03	thyroid tumor, adenoma, 28 F	1	0.0138		

FIGURE 5

10/10